



; VOLUME: 84  
 ; PAGES: 5555-5559  
 ; DATE: 1987  
 ; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 3048  
 US-08-313-200-2

```

alignment_scores:
  Quality: 4528.00      Length: 848
  Ratio: 5.365          Gaps: 0
  Percent Similarity: 99.528  Percent Identity: 99.175

alignment_block:
  US-08-482-402A-3_COPY_1_848 x US-08-313-200-2 ..

Align seq 1/1 to: US-08-313-200-2 from: 1 to: 3048

```

```
alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-313-200-2 ..
```

Align seq 1/1 to: US-08-313-200-2 from: 1 to: 3048

1 MetArgAlaLeuAlaValLeuSerValThrLeuValMetAlaCysThrG1 17  
73 ATGAGAGCGCTCGCTGCTGCTGCTCAGCTGCTTATGGCTGCACAGA 122

17 uAlaPhePhePropHeIleSerArgGlyLysGluLeuLeuThrpgGlyLysP 34  
123 AGCCCTTCTTCCCTTCATCTCGAGAGGGAAGAAGAACTCCTTTGGGAAAGC 172

34 roGluGluSerArgValSerSerValLeuGluGluSerLysArgLeuVal 50  
173 CTGAGAGAGTCTCGTGCTCTAGCGCTCTGGAGGAAAGCAAGCGCTGGTG 222

51 AspThrAlaMetTyrAlaThrMetGlnArgAsnLeuLysLysArgGlyI1 67  
223 GACACGGCCATGTACGCCAGATGCAGAGAAACCTCAAGAAAGAGGAAT 272

67 eLeuSerGlyAlaGlnLeuLeuSerPheSerLysLeuProGluProThrS 84  
273 CCTTCTCCAGCTCAGCTCTGCTCTTTTCCAAACTTCCCTGAGCCAACA 322

84 erGlyValIleAlaArgAlaAlaGluIleMetGluThrSerIleGlnAla 100  
323 GCGGAGTGATTGCCGAGCAGCAGAGAGATAATGGAACAATCAATCAAGCG 372

101 MetLysArgLysValAsnLeuLysThrGlnGlnSerGlnHisProThrAs 117  
373 ATGAAAGAAAAAGTCAACCTGAAAACTCAACAATCAGACGATCCAACGGA 422

117 pAlaLeuSerGluAspLeuLeuSerIleIleAlaAsnMetSerGlyCysL 134  
423 TGCCTTATCAGAAGATCTGCTGAGCATCATGTGCAACAATGTCTGATGTC 472

134 euProTyrMetLeuProProLysCysProAsnThrCysLeuAlaAsnLys 150  
473 TCCCTTTACATGCTGCCCCCAAAATGCCCAACACTTGCCTGGCGAACAAA 522

151 TyrArgProIleThrGlyAlaCysAsnAsnArgAspHisProArgTgPrG1 167

|       |  |      |
|-------|--|------|
| 234   | lyGlnTyrIleAspHisAspIleAlaPheThrProGlnSerThrSerLys     | 250  |
| 773   | GACAATACATCGACCGACGACATCGCGTTACACACAGACACACGACAA       | 822  |
| 251   | AlaAlaPheGlyGlySerAspCysGlnMeIThrCysGluAsnGlnAs        | 267  |
| 823   | GCTGCCCTTCGGGGAGGGGTGACTGCCAGATGACTTGTGAGAACCAAA       | 872  |
| 267   | nProCysPheProIleGlnLeuProGluGluAlaArgProAlaAlaGlyT     | 284  |
| 873   | CCCATGTTTCCCATACAACCTCCGGAGGAGCGCGCCGCCCGCGGCA         | 922  |
| 284   | hrAlaCysLeuProPheTyrArgSerSerAlaAlaCysGlyThrGlyAsp     | 300  |
| 923   | CCGCGCTCTCGCGCTTCTACCGCTCTTTCGGCGCGCTCGGCACCGGGAC      | 972  |
| 301   | GlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMe     | 317  |
| 973   | CAAGCGCGCTCTTTGGGAACCTGTCCACGGCCAACCCGGCGGACGAGAT      | 1022 |
| 317   | tAsnGlyLeuThrSerPheLeuAspAlaSerThrValTyrGlySerSerP     | 334  |
| 11023 | GAACGGGTTCACCTCGTTCTCTGGACGGCTCACCGTGTATGGCAGCTCC      | 1072 |
| 334   | roAlaLeuGluArgGlnLeuArgAsnTrpThrSerAlaGluGlyLeuLeu     | 350  |
| 11073 | CGGCCCTTAGAGAGCGACGTCCGGAACTTGGACACAGTTCGCGAAGGGCTGCTC | 1122 |
| 351   | ArgValHisGlyArgLeuArgAspSerGlyArgAlaTyrLeuProPheVa     | 367  |
| 11123 | CGGTCCACGCGCGCTTCGGGGACTTCGGCGCGCTTACCTGCCCTTCGT       | 1172 |
| 367   | lProProArgAlaProAlaAlaCysAlaProGluPuProGlyAsnProGlyG   | 384  |
| 11173 | GCCGCCACGGCGGCTTCGGCGCTTCGGCCCGACCCGGCGATCCCGCGAG      | 1222 |
| 384   | luThrArgGlyProCysPheLeuAlaGlyAspGlyArgAlaSerGluVal     | 400  |
| 11223 | AGACCCCGGGCGCTGTCTCTTCGGCGGAGACGCGCGCGCCACGCGAGTCT     | 1272 |
| 401   | ProSerLeuThrAlaLeuHisThrLeuTrpLeuArgGluHisAsnArgLe     | 417  |
| 11273 | CCCTTCCCTGACGGCATTGCACACGCTGTGGCTGGCGGAGCACAAACCGCCT   | 1322 |
| 417   | uAlaAlaAlaLeuLysAlaLeuAsnAlaHisTrpSerAlaAspAlaValT     | 434  |
| 11323 | GGCGCGGGCGCTCAAGGCCCTCAATGGCCTGGAGCGCGGACGCGGTGT       | 1372 |
| 434   | yrGlnGluAlaArgLysValValGlyAlaLeuHisGlnIleIleThrLeu     | 450  |
| 11373 | ACCAGGAGCGCGCAAGTCTGTGGCGCTCTGCACACAGATCATCACCTGT      | 1422 |
| 451   | ArgAspTyrIleProArgIleLeuGlyProGluAlaPheGlnGlnTrpVa     | 467  |
| 11423 | AGGGATTATATCCCAAGATTCTTGGACCCGAGCGCTTCACAGACATCGT      | 1472 |
| 467   | lGlyProTyrGluGlyTyrAspSerThrAlaAsnProThrValSerAsnV     | 484  |
| 11473 | GGGTCCCTATGAGGCTATGACTCCACCGCCCAACCCCACTGTGTCCACG      | 1522 |
| 484   | alPheSerThrAlaAlaPheArgPheGlyHisAlaThrIleHisProLeu     | 500  |
| 11523 | TGTTCTCCACAGCGCGCTTCCGCTTCGGCCATGCCAGATCCACCGCTGT      | 1572 |
| 501   | ValArgArgLeuAspAlaSerPheGlnGluHisProAspLeuProGlyLe     | 517  |
| 11573 | GTGAGGAGGTGGACGCCAGCTTCCAGGAGCACCCCGACCTGCCCGGGCT      | 1622 |
| 517   | uTrpLeuHisGlnAlaPhePheSerProTrpThrLeuLeuArgGlyClyG     | 534  |
| 11623 | GTGGCTCCACAGGCTTCTTCAGCCCATGGACATTACTCCGTGGAGGTG       | 1672 |
| 534   | lyLeuAspProLeuIleArgGlyLeuLeuAlaArgProAlaLysLeuGln     | 550  |

|||||  
1673 GTTGGACCCACTAATACGAGCCCTTCTGCAAGACCAACCCAACTGCAG 1722  
551 ValGlnAspGlnLeuMetAsnGluGluLeuThrGluArgLeuPheValLe 567  
1723 GTGCAGGATCAGCTGATGAACAGAGAGCTGACGGAAGGCTCTTTGTGCT 1772  
567 uSerAsnSerThrLeuAspLeuAlaSerIleAsnLeuGlnArgGlyA 584  
1773 GTCCAATCCAGCACCTTGATCTGGCGTCCATCAACCTGCAGAGGGCC 1822  
584 rAspHisGlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeu 600  
1823 GGGACACCGGCTGCAGGTTACAATGATGAGGAGGAGTCTCGCGCCTG 1872  
601 ProArgLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSe 617  
1873 CCTCGCCTGGAGACCCCGCTGACTGAGCAGACCCATCGCCAGCAGAG 1922  
617 rValAlaAspLysIleLeuAspLeuTyrLysHisProAspAsnIleAspV 634  
1923 CGTGGCCGACAGATCTCGGACTGTACAAAGCATCCTGACAAACATCGATG 1972  
634 alTrpLeuGlyGlyLeuAlaGluAsnPheLeuProArgAlaArgThrGly 650  
1973 TCTGGCTGGGAGGCTTAGCTCAAAACTTCTCCCGCAGGCTCGGACAGGG 2022  
651 ProLeuPheAlaCysLeuIleGlyLysGlnMetLysAlaLeuArgAspG 667  
2023 CCCCTGTTTGGCTGTCTCATTTGGGAAGCAGATGAAGGCTCTCGCGGATGG 2072  
667 yAspTrpPheTrpTrpGluAsnSerHisValPheThrAspAlaGlnArgA 684  
2073 TGACTGGTTTGGTGGGAGAACACCGACCTCTTACGGATGCACAGAGC 2122  
684 rGluLeuGluLysHisSerLeuSerArgValIleCysAspAsnThrGly 700  
2123 GTGAGCTGGAGAAGCACTCCCTGCTCTCGGTCATCTGTGACAACACTGGC 2172  
701 LeuThrArgValPrometAspAlaPheGlnValGlyLysPheProGluAs 717  
2173 CTCACCGGGTGGCCATGGATGGCTTCCAACTCGGCAAAATTCCTTGAAGA 2222  
717 pPheGluSerCysAspSerIleThrGlyMetAsnLeuGluAlaTrpArgG 734  
2223 CTTTGAGTCTTGTGACACATCCCTGGCATGAACCTGGAGCCCTGGAGGG 2272  
734 luThrPheProGlnAspLysCysGlyPheProGluSerValGluAsn 750  
2273 AAACCTTTCTCAAGACGACAAAGTGGCTCTCCAGAGAGCGTGAGAAAT 2322  
751 GlyAspPheValHisCysGluGluSerGlyArgArgValLeuValTrpSe 767  
2323 GGGGACTTTGTGCATCTGTGAGGAGTCTGGGAGGCGGTGCTGTATTTC 2372  
767 rCysArgHisGlyTyrGluLeuGlnGlyArgGluGlnLeuThrCysThrG 784  
2373 CTGCGCGGACGGGATGAGTCCAAAGCCGGGAGCAGCTCACTTGACCCC 2422  
784 lngLuglyTrpAspPheGlnProProLeuCysLysAspValAsnGluCys 800  
2423 AGGAAGGATGGATTTCAGCGCTCCCTCTGCAAGATGTGAACAGTGT 2472  
801 AlaAspGlyAlaHisProProCysHisAlaSerAlaArgCysArgAsnTh 817  
2473 GCAGACGGTGCCACCCCGCTGCGACGCCCTCTGCGAGGTGCAGAAACAC 2522  
817 rLysGlyGlyPheGlnCysLeuCysAlaAspProTyrGluLeuGlyAspA 834  
2523 CAAAGCGGCTTCCAGTGCTCTCTCGCGGACCCCTTACGAGTTAGGAGAG 2572  
834 spGlyArgThrCysValAspSerGlyArgLeuProArgValThr 848  
|||||

2573 ATGGGAGAACCTGGTAGACTCCGGGAGGGCTCCTCGGGGACT 2616  
seq\_name: /cgn\_2\_6/ptodata/2/1na/PCTUS\_COMB.seq:PCT-US93-03837-2  
seq\_documentation\_block:  
; Sequence 2, Application PC/TUS9303837  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Jr., James R.  
; APPLICANT: Koenig, Ronald J.  
; TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/03837  
; FILING DATE: 19930422  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lewak, Anna M.  
; REGISTRATION NUMBER: 33006  
; REFERENCE/DOCKET NUMBER: 2115-00658PPA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (313) 641-1600  
; TELEFAX: (313) 641-0270  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3048 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; DEVELOPMENTAL STAGE: Mature  
; TISSUE TYPE: Thyroid gland (from patients with  
; TISSUE TYPE: Grave's disease)  
; IMMEDIATE SOURCE:  
; CLONE: pHTPO-2.8  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: 2pter-q11  
; PUBLICATION INFORMATION:  
; AUTHORS: Kimura, S.  
; AUTHORS: Kotani, T.  
; AUTHORS: McBride, O. W.  
; AUTHORS: Umeki, K.  
; AUTHORS: Nakayama, T.  
; AUTHORS: Ohtaki, S.  
; AUTHORS: Hirai, K.  
; TITLE: Human thyroid peroxidase: Complete cDNA and  
; TITLE: protein sequence, chromosome mapping, and  
; TITLE: identification of two alternately spliced mRNAs  
; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
; VOLUME: 84  
; PAGES: 5555-5559  
; DATE: 1987  
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 3048  
PCT-US93-03837-2

alignment\_scores: Quality: 4528.00 Length: 848

Ratio: 5.365 Gaps: 0  
Percent Similarity: 99.528 Percent Identity: 99.175  
alignment\_block:  
US-08-482-402a-3\_copy\_1\_848 x PCT-US93-03837-2 ..  
Align seg 1/1 to: PCT-US93-03837-2 from: 1 to: 3048

1 MetArgAlaLeuAlaValLeuSerValThrLeuValMetAlaCysThrGl 17  
73 ATGAGAGCGCTCGGTGCTCTCTACGCTCTTGGAGAAAGCAAGCGCTGGTGCACAGA 122  
17 uAlaPhePheProPheIleSerArgGlyLysLeuLeuLeuTrpGlyLysP 34  
123 AGCCTTCTCCCTCTCAFTCTCGAGAGGAAAGAACTCCTTTGGGAAAGC 172  
34 roGluGluSerArgValSerSerValLeuGluGluSerLysArgLeuVal 50  
173 CTGAGGAGTCTCGTGTCTCTAGCGTCTTGGAGAAAGCAAGCGCTGGTG 222  
51 AspThrAlaMetTyrAlaThrMetGlnArgAsnLeuLysLysArgGlyI 67  
223 GACACCGGCATGTACGCCACGATGCAGAGAAACCTCAAGAAAGAGGAAT 272  
67 eLeuSerGlyAlaGlnLeuLeuSerPheSerLysLeuProGluProThrS 84  
273 CCTTCTCCACCTCAGCTTCGTCTCTTTTCCAAACTTCTGAGCCAAACA 322  
84 erGlyValIleAlaArgAlaAlaGluIleMetGluThrSerIleGlnAla 100  
323 CGGAGTGATTGCCCGACACAGAGATAATGGAAACATCAATACAGCG 372  
101 MetLysArgLysValAsnLeuLysThrGlnGlnSerGlnHisProThrAs 117  
373 ATGAAAGAAAGTCAACTCAAACTCAACAATCACAGATCCCAACGGA 422  
117 pAlaLeuSerGluAspLeuLeuSerIleIleAlaAsnMetSerGlyCysL 134  
423 TGCCTTATCAGAAGATCTGCTGAGCATCATTCGCAAAACATGTCTGGATGTC 472  
134 euProTyrMetLeuProProLysCysProAsnThrCysLeuAlaAsnLys 150  
473 TCCCTTACATGCTGCCCCCAAAATGCCCAACACTTGCTGCGCAACAAA 522  
151 TyrArgProIleThrGlyAlaCysAsnAsnArgAspHisProArgTrpGl 167  
523 TACAGGCCCATCACAGAGCTTGGCAACACAGAGACCAACCCAGATGGG 572  
167 yAlaSerAsnThrAlaLeuAlaArgTrpLeuProProValTyrGluAspG 184  
573 CGCCTCCAACACGGCCCTGGCAGCATGCTCCCTCCAGTCTATGAGGAGC 622  
184 lypHeSerGlnProArgGlyTrpAsnProGlyPheLeuTyrAsnGlyPhe 200  
623 GCTTCAGTCAAGCCCGAGGCTGGAAACCCCGCTTCTTGTACAACGGGTC 672  
201 ProLeuProProValArgGluValThrArgHisValIleGlnValSerAs 217  
673 CCACTGCCCGCGTCCGGAGGCTGACACAGACATGTCATTCAAGTTTCAAA 722  
217 nGluValValThrAspAspArgTyrSerAspLeuLeuMetAlaIatrpG 234  
723 TGAGGTTGTACAGATGATGACCGCTATTCTGACCTCTCTGATGGCATGG 772  
234 lyGlnTyrIleAspHisAspIleAlaPheThrProGlnSerThrSerLys 250  
773 GACAATACATCGACACGACATCGCGTTTCAACACACAGAGCACCAGCAAA 822  
251 AlaAlaPheGlyGlySerAspCysGlnMetThrCysGluAsnGlnAs 267  
823 CTGCTTCGGGGAGGGGCTGACTGCCAGATGACTTGTGAGAACCAAAA 872  
267 nProCysPheProIleGlnLeuProGluAlaAlaArgProAlaAlaGlyT 284

873 CCCATGTTTCCCATACAACTCCCGGAGGAGCCCGCGCGCGCGGCA 922  
284 hrAlaCysLeuProPheTyrArgSerSerAlaAlaCysGlyThrGlyAsp 300  
923 CGGCTGTCTGCGCTTCTACCGCTCTTCGGCGGCTTCGGCACCGGGGAC 972  
301 GlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMe 317  
973 CAAGGCGCGCTCTTTGGAAACCTGTCCACGGCAACCCCGCGGACAGAT 1022  
317 tAsnGlyLeuThrSerPheLeuAspAlaSerThrValTyrGlySerSerP 334  
1023 GAACGGGTTGACCTCGTCTCTGACGCGCTCCACCGTGTATGGCAGCTCC 1072  
334 roAlaLeuGluArgGlnLeuArgAsnTrpThrSerAlaGluGlyLeuLeu 350  
1073 CGGCGCTAGAGAGGACGTGCGGAACCTGGACAGTCCCGAAGGCTGCTC 1122  
351 ArgValHisGlyArgLeuArgAspSerGlyArgAlaTyrLeuProPheVa 367  
1123 CGGCTCCACGCGCGCTTCGGGACTCCGGCGCGCTACCTGCGCTTCGT 1172  
367 lProProArgAlaProAlaAlaCysAlaProGluProGlyAsnProGlyG 384  
1173 GCGGCCACGCGCGCTTCGGCGCTTCGGCGCGCGCGCGCATCCCGGAG 1222  
384 luThrArgGlyProCysPheLeuAlaGlyAspGlyArgAlaSerGluVal 400  
1223 AGACCGCGCGCGCTTCCTGCGCGGAGAGCGCGCGCGCAGGAGTGC 1272  
401 ProSerLeuThrAlaLeuHisThrLeuTrpLeuArgGluHisAsnArgLe 417  
1273 CCCTCCCTGACGCGACTGCACACGCTGTGCTGGCGAGGACCAACCGCT 1322  
417 uAlaAlaLeuLysAlaLeuAsnAlaHisTrpSerAlaAspAlaValT 434  
1323 GCGCGCGCGCTCAAGCGCTCAATCGCACTGGAGCGCGCGCGCGCTGT 1372  
434 yGlnGluAlaArgLysValValGlyAlaLeuHisGlnIleIleThrLeu 450  
1373 ACCAGAGGCGCGCAAGTGTGGCGCTTCGACACGATCATCACCTG 1422  
451 ArgAspTyrIleProArgIleLeuGlyProGluAlaPheGlnTrpVa 467  
1423 AGGATTACATCCCCAGGATCTTCGGACCGCGCGCTTCACAGCAGTACGT 1472  
467 lGlyProTyrGluGlyTyrAspSerThrAlaAsnProThrValSerAsnV 484  
1473 GGTCTCCCTATGAAGGCTATGACTCCACCGCAACCCACTGTGTCCAACG 1522  
484 aIpeSerThrAlaAlaPheArgPheGlyHisAlaThrIleHisProLeu 500  
1523 TGTTCCTCCACGCGCTTCGCTTCGGCATGCCAGCATCCACCGCTG 1572  
501 ValArgArgLeuAspAlaSerPheGlnGluHisProAspLeuProGlyLe 517  
1573 GTGAGGAGGCTGGACCGCAGCTTCAGGAGCACCCCGACCTGCCCGGCT 1622  
517 uTrpLeuHisGlnAlaPhePheSerProTrpThrLeuLeuArgGlyGly 534  
1623 GTGGCTGCACCGCTTCTTTCAGCCATGGACATTTACTCCGTGGAGGTG 1672  
534 lyleuAspProLeuIleArgGlyLeuLeuAlaArgProAlaLysLeuGln 550  
1673 GTTGGACCCACTAATACAGGCGCTTCTTGAAGACCAAGCAAACTGCAG 1722  
551 ValGlnAspGlnLeuMetAsnGluGluLeuThrGluArgLeuPheValIe 567  
1723 GTGAGGATCAGCTGATGAACGAGGAGCTGACGGAAGGCTCTTTGTGCT 1772  
567 uSerAsnSerSerThrLeuAspLeuAlaSerIleAsnLeuGlnArgGlyA 584

1773 GTCCAAATCCAGACCTTGATCTGGCGTCCATCAACCTGCAGAGGGGCC 1822  
584 rAspHisGlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeu 600  
1823 GGGACACGGCTGCCAGGTTACAATGAGTGGAGGAGTTCTGGGGCTG 1872  
601 ProArgLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSe 617  
1873 CCTCGCTGGAGACCCCGCTGACCTGAGCACACGCCATGCCAGCAGGAG 1922  
617 rValAlaAspLysIleLeuAspLeuTyrLysHisProAspAsnIleAspV 634  
1923 CGTGGCGCAAGATCTGACCTGTACAAAGCATCTCGACAACATCGATG 1972  
634 alTrpLeuGlyGlyLeuAlaGluAsnPheLeuProArgAlaArgThrGly 650  
1973 TCTGGCTGGAGGCTTAGCTGAANAACCTTCTCCCGAGGGCTCGGACAGG 2022  
651 ProLeuPheAlaCysLeuIleGlyLysGlnMetLysAlaLeuArgAspGl 667  
2023 CCCCTGTTGCCCTGCTCAATTGGAGACAGATGAAGCTCTGGGGATGG 2072  
667 yAspTrpPheTrpTrpGluAsnSerHisValPheThrAspAlaGlnArgA 684  
2073 TGACTGTTTTTGGTGGAGAACAGCCACGCTTTTCACGGATGCACAGAGC 2122  
684 rGluLeuGluLysHisSerLeuSerArgValIleCysAspAsnThrGly 700  
2123 GTGAGCTGGAGAGCATCTCCTGTCTGGGTCACTGTGACAACACTGGC 2172  
701 LeuThrArgValProMetAspAlaPheGlnValGlyLysPheProGluAs 717  
2173 CTCACAGGCTGCCATGGATGCTTCCAAAGTCGGCAAAATCCCTGAAGA 2222  
717 pPheGluSerCysAspSerIleThrGlyMetAsnLeuGluAlaTrpArgG 734  
2223 CTTTGAGTCTGTGACAGCATCTCCTGGCATGAACCTGGAGGCTTGGAGG 2272  
734 luThrPheProGlnAspLysCysGlyPheProGluSerValGluAsn 750  
2273 AAACCTTCTCAAGACGACAAGTGTGGCTTCCAGAGAGCGTGGAGAAT 2322  
751 GlyAspPheValHisCysGluGluSerGlyArgValLeuValTyrSe 767  
2323 GGGACTTTGTGCACCTGTGAGGAGTCTGGAGGCGCTGTGTGTATTC 2372  
767 rCysArgHisGlyTyrGluLeuGlnGlyArgGluGlnLeuThrCysThrG 784  
2373 CTGCGGCACGGGTATGAGCTCCAAGGCGGGAGCAGCTCACTTGCACCC 2422  
784 lngLuGlyTyrAspPheGlnProProLeuCysLysAspValAsnGluCys 800  
2423 AGGAAGATGGGATTTCCAGCTCCCTCTGCAAAAGATGTGAACGAGTGT 2472  
801 AlaAspGlyAlaHisProProCysHisAlaSerAlaArgCysArgAsnTh 817  
2473 GCAGACGGTCCCAACCCCTGCCAGCCCTCTGCGAGGTGCAGAAACAC 2522  
817 rLysGlyGlyPheGlnCysLeuCysAlaAspProTyrGluLeuGlyAspA 834  
2523 CAAAGGGGCTTCCAGTGTCTCTGCGGGGACCCCTACGAGTGTAGGAGCG 2572  
834 spGlyArgThrCysValAspSerGlyArgLeuProArgValThr 848  
2573 ATGGGAGAACCTCGTAGACTCCGGGAGGCTCCCTCGGGGGACT 2616

seq\_name: /cgn2\_6/ptodata/2/ina/backfiles1.seq:5460961-1  
seq\_documentation\_block:  
; Patent No. 5460961  
; APPLICANT: DEBY, CAROL; PINGEMAIL, JOEL; BOLLEN, ALEX  
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS  
; THERAPEUTIC APPLICATION

; NUMBER OF SEQUENCES: 13  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/641,678  
; FILING DATE: 16-JAN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 460,931  
; FILING DATE: 14-FEB-1990  
; SEQ ID NO:1:  
; LENGTH: 2261  
5460961-1  
  
alignment\_scores:  
Quality: 1576.50 Length: 749  
Ratio: 3.014 Gaps: 11  
Percent Similarity: 69.826 Percent Identity: 42.857  
  
alignment\_block:  
US-08-482-402A-3\_COPY\_1\_848 x 5460961-1 ..  
  
Align seg 1/1 to: 5460961-1 from: 1 to: 2261

1 MetArgAlaLeuAlaValLeuSerValThrLeuValMetAlaCysThrGl 17  
87 ATGAAGCTGCTTCTGGCCCTAGCAGCGCTCCTGGCCATTCTGCCACG.. 134  
17 uAlaPhePheProPheIleSerArgGly...LysGluLeuLeuTrpGlyL 33  
135 .....CCCCAGCCCTCTGAAGGTGCTGCTCCAGCTGCTCTGGGGG 174  
33 ysProGluGluSerArgValSerSerValLeuGluGluSerLysArgLeu 49  
175 AGGTGGACACCTCGTGTGTGCTGAGCTCCATGAGGAGGCCAAGCAGCTG 224  
50 ValAspThrAlaMetTyrAlaThrMetGlnArgAsnLeuLysLysArg.. 65  
225 GTGGACAAGGCC...TAGAAGGAGGCGGGGAAAGCATCAAGCAGCGGCT 271  
66 .....GlyIleLeuSerGlyAlaGlnLeuLeuSerPheSerLysLeuP 80  
272 TCGCAGCGGCTCAGCCAGCCCATGGAACTCCTATCTACTTCAAGCAGC 321  
80 roGluProThrSerGlyValIleAlaArgAlaAlaGluIleMetGluThr 96  
322 CGGTGGCAGCCACAGGCGCGGTGAGGCGCGCTGACTACCTGCACGTG 371  
97 SerIleGlnAlaMetLysArgLysValAsnLeuLysThrGlnGlnSerGl 113  
372 GCTCTAGACCTGCTGGAGAGGAAGCTGCGGTCCCTGTGGCGAAGGCCA 421  
113 nHisProThrAspAlaLeuSerGluAspLeuSerIleIleAlaAsnM 130  
422 CAATGCTACTGATGTGTACGCCCGCCAGCTGAATGTGTGTCCAAGT 471  
130 etSerGlyCysLeuProTyrMetLeuProProLysCysProAsnThrCys 146  
472 CAAGCGGTGCGCCTACCAGGACGTGGGGGTGACTTGCCCGGAG..... 515  
147 LeuAlaAsnLysTyrArgProIleThrGlyAlaCysAsnAsnArgAspHi 163  
516 ...CAGGACAAATACCGCACCATCACCGGGATGTGCAACAACAGAGCGCAG 562  
163 sProArgTrpGlyAlaSerAsnThrAlaLeuAlaArgTrpLeuProProv 180  
563 CCCACGCTGGGGGCTCCACACCGTGCCTTTGTGGCTGGCTGCCGCGCG 612  
180 alTyrGluAspGlyPheSerGlnProArgGlyTrpAsnProGlyPheLeu 196  
613 AGTATGAGGAGCGGCTTCTCTCTCCCTACGCTGGACGCCCGGGGTCAAG 662  
197 TyrAsnGlyPheProLeuProProValArgGluValThrArgHisValI 213  
663 CGCAACGGCTTCCCGGTGGCTGTGGCTCGCGGGTCTCCCAACGAGATCGT 712

```
213 eGlnValSerAsnGluValValThrAspAspArgTyrSerAspLeuL 230
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
713 GCGCTTCCCACTGATCAGCTGACTCGGACCGAGCGCTCACTCATGT 762
230 euMetAlaTrpGlyGlnTyrIleAspHisAlaPheThrProGln 246
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
763 TCATGCAATGGGGCCAGCTGTGGACGACGACCTCGACTCCACCCCTGAG 812
247 SerThrSerIysAlaAlaPheGlyGlySerAspCysGlnMetThrCy 263
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
813 CCGCGCCCGCGGCTCCTTCGTCTAGTGGCTCACTGCGAGACGAGCTG 862
263 sGluAsnGlnAsnProCysPheIleGlnLeu...ProGluAlaAla 279
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
863 CGTTTCAGCAGCGCCCTTCCTCCGCTCAAGATCCGCGCCCAATGACCCC 912
279 rgProAlaAlaGlyThrAlaCysLeuProPheTyrArgSerSerAlaAla 295
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
913 GCATCAAGAAACCAAGCGAGCTGCATCCGTTCTTCCGCTCCTGCCGCT 962
296 CysGlyThrGlyAspGlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAs 312
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
963 TGCCCCGGG.....AGCAACATCAC 982
312 nProArgGlnGlnMetAsnGlyLeuThrSerPheLeuAspAlaSerThrV 329
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
983 CATCCGCAACAGATCAACGGCTCACTTCCTCGTGACCGCCAGCATGG 1032
329 alTyrGlySerSerProAlaLeuGluArgGlnLeuArgAsnTrpThrSer 345
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1033 TGTACGGCAGCGAGGAGCGCTGGCCAGGACCTGCGCAACATGTCCAAC 1082
346 AlaGluGlyLeuLeuArgValHisGlyArgLeuArgAspSerGlyArgAl 362
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1083 CAGTGGGGCTGTGGCGCTCAACAGCGCTTCCAAGACAACGCGCGGC 1132
362 atYLeuProPhe.....ValProProA 370
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1133 CTGCTGCCCTTTGCACACCTGCAGATGACCCCTGCTCTCTCACCAC 1182
370 rgAlaProAlaAlaCysAlaProGluProGlyAsnProGlyGluThrArg 386
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1183 GCTCA.....GCGGC 1193
387 GlyProCysPheLeuAlaGlyAspGlyArgAlaSerGluValProSerLe 403
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1194 ATCCCTGCTTCTGGCAGGGGACACCCGTTCCAGTGAGATGCCCGAGCT 1243
403 uThrAlaLeuHisThrLeuTrpLeuArgGluHisAsnArgLeuAlaAla 420
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1244 CACTCCATGCACACCTCTTACTTCGGGACCAACCGCGTGGCCACAG 1293
420 laLeuLysAlaLeuAsnAlaHisTrpSerAlaAspAlaValTyrGlnGlu 436
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1294 AGCTCAAGAGCTCAACCTAGGTGGGATGGGAGAGGCTCTACCAAGAA 1343
437 AlaArgLysValValGlyAlaLeuHisGlnIleLeuLeuArgAspTy 453
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1344 GCCCGAAGATCGTGGGGCCATGCTCCAGATCATCACTTACCAGGACTA 1393
453 rIleProArgIleLeuGlyProGluAlaPheGlnGlnTyrValGlyProt 470
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1394 CTTCCCTGTGTGGGCGCAACGGCATGAGGAAGTACCTGCCACAGT 1443
470 yrGluGlyTyrAspSerThrAlaAsnProThrValSerAsnValPheSer 486
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1444 ACCGTTCTCAATGACTCAGTGGACCCACCCATCGCAACGCTTC... 1490
487 ThrAlaAlaPheArgPheGlyHisAlaThrIleHisProLeuValArgAr 503
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1491 ACCAATGCTTCCGCTACGGCCACACCCCTCATCCAACCTTCATGTTCCG 1540

503 gLeuAspAlaSerPheGlnGluHisProAspLeuProGlyLeuTrpLeuH 520
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1541 CTGGACAATCGTACCACCCATGGAACCAACCCCGTGTCCCTCA 1590
520 isGlnAlaPhePheSerProTrpThrLeuLeuArgGlyGlyGlyLeuAsp 536
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1591 GAGGGTCTTTTTCCTGCTGGAGGCTGCTGGAAGGTGGCATGTGAC 1640
537 ProLeuIleArgGlyLeuLeuAlaArgProAlaLysLeuGlnValGlnAs 553
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1641 CCATCTCTCCGGGGCTCATGCCACCCCTGCAAGCTGAATCGTCAGAA 1690
553 pGlnLeuMetAsnGluGluLeuThrGluArgLeuPheValLeuSerAsnS 570
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1691 CCAATTCAGTGGATGAGATCCGGGAGCGATTGTTTGAGCAGGTCA 1740
570 erSerThrLeuAspLeuAlaSerIleAsnLeuGlnArgGlyArgAspHis 586
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1741 GGATTGGGCTGGACCTGCTGCTGAACATCGAGCGCAGCAGGACCAC 1790
587 GlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeuProArgLe 603
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1791 GCCCTCCAGGATACATCCCTGGAGCGCTTCTGTGGCTCCCGAGCC 1840
603 uGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSerValAlaA 620
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1841 TGAACATGTGGGCCAGCTGGGACCGGTGTGAGGAACCTGAATTTGCCGA 1890
620 sPlysIleLeuAspLeuTyrLysHisProAspAsnIleAspValTrpLeu 636
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1891 GGAAATCGATGGAGCAGTAGTGGCACGCCCAACCAACATCGACATCTGGATG 1940
637 GlyGlyLeuAlaGluAsnPheLeuProArgAlaArgThrClyProLeuPh 653
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1941 GCGCGCTGTCCGAGCTTGAAGCGCAAGGCGCGTGGGCGCCACTCCT 1990
653 eAlaCysLeuIleGlyLysGlnMetLysAlaLeuArgAspGlyAspTrpP 670
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1991 CCGCTGCATCATCGTACCCAGTTCAGGAAGTCCCGGATGGTGATCGGT 2040
670 heTrpTrpGluAsnSerHisValPheThrAspAlaGlnArgArgGluLeu 686
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
2041 TTTGTGGGAGAACGAGGTGTCTCAGCATGCAGCAGCAGCAGGCGCTG 2090
687 GluLysHisSerLeuSerArgValIleCysAspAsnThrGlyLeuThrAr 703
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
2091 GCCCATGTCATTCATGCCCGATCATCTCGACACACACAGGCATCCAC 2140
703 gValProMet...AspAlaPheGlnValGlyLysPheProGluAspPheG 719
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
2141 CGTGCTTAGAACACACATCTTTCATGTCCAACTCATATCCCGGACTTGG 2190
719 luSerCysAspSerIleThrGlyMetAsnLeuGluAlaTrpArgGlu 734
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
2191 TCAACTGCAGTACACTTCCTGCATTCGAACCTGGCTTCCTCGAGGAA 2237

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5460961-4
seq_documentation_block:
; Patent No. 5460961
; APPLICANT: DEBY, CAROL; PINCEMAIL, JOEL; BOLLEN, ALEX
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
; THERAPEUTIC APPLICATION
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,678
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 460,931
; FILING DATE: 14-FEB-1990
; SEQ ID NO:4
; LENGTH: 2097
5460961-4
```



```
1582 GTCATGAGGATTGGCTGGAGCTGGGTGCTCTGAACATGCGACGCGAGCAG 1631
584 gAspHisGlyLeuProGlyTyTrpAsnGluTrpArgGluPheCysGlyLeuP 601
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1632 GGACACGGCTCCAGGATACATGCTCGAAGCGCTTCTGTGGCTCC 1681
601 roArgLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSer 617
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1682 CGCAGCCTGAAGACTGTGGCCAGCTGGCGAGTGGCGGTGCTGAGGAACCTGAA 1731
618 ValAlaAspLysIleLeuAspLeuTyTrpLysHisProAspAsnIleAspVa 634
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1732 TTGGCGGAAGAACTGATGGAGCAGTATGGCAGCCCAACACATCGACAT 1781
634 lTrpLeuGlyGlyLeuAlaGluAsnPheLeuProArgAlaArgThrGlyP 651
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1782 CTGGATGGCGCGGTGTCGAGCCTCTGAAGCGCAAGCGCGGTGGAC 1831
651 roLeuPheAlaCysLeuIleGlyLysGlnMetLysAlaLeuArgAspGly 667
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1832 CACTCCTCGCCTGCATCATCGGTACCCAGTTCAGGAAGCTCGGGATGCT 1881
668 AspTrpPheTrpTrpGluAsn.SerHisValPheThrAspAla.GlnArg 683
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1882 GATCGGTTTGGTGGGAGAACGAGGGGTGTGTTCAGCAATGCAGACGCA 1931
684 ArgGluLeuGluLysHisSerArgValIleCysAspAsnThr.G 700
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1932 CAGGCGCTGGCCCGCATCATGTCGCCGGATCATCTCGGACACACAG 1981
700 lyLeuThrArgValProMet...AspAlaPheGlnValGlyLysPhePro 715
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1982 GCATCACCACCGTGTCTAAGAACACATCTTCATGTCCAACATCATATCC 2031
716 GluAspPheGluSerCysAspSerIleThrGlyMetAsnLeuGluAlaTr 732
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2032 CGGGACTTTGTCAACTGCAGTACATCTCTGCATTTGAACCTGGCTCTCTG 2081
732 pArgGlu 734
|||||
2082 GAGGAA 2088
seq_name: /cgn2_5/ptodata/2/ina/6A_COMB.seq:us-08-840-551-7
seq_documentation_block:
; Sequence 7, Application US/08840551B
; Patent No. 6066449
; GENERAL INFORMATION:
; APPLICANT: Dittkoiff, Beth A., et al.
; TITLE OF INVENTION: METHOD OF DETECTING METASTATIC THYROID CANCER
; FILE REFERENCE: 0575/51662/jpw/jkm
; CURRENT APPLICATION NUMBER: US/08/840,551B
; CURRENT FILING DATE: 1997-04-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: OTHER NUCLEIC
US-08-840-551-7
```

```
alignment_scores:
  Quality: 396.00      Length: 105
  Ratio: 4.659
Percent Similarity: 80.952  Percent Identity: 76.190
alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-840-551-7/rev ..
```

```
Align seg 1/1 to reverse of: US-08-840-551-7 from: 1 to: 262
76 PheSerLysLeuProGluProThrSerGlyValIleAlaArgAlaAlaG1 92
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
261 TTTTCCAAACTTCTGAGCCAAACAGCGGAGTGATTCCCGCAGCAGCA 212
92 uIleMetGluThrSerIleGlnAlaMetLysArgLysValAsnLeuLysT 109
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
211 GATAATGGAAACATCAATACAAGCGATGAAAGAAAGTCAACCTGAAAA 162
109 hrGlnGlnSerGlnHisProThrAspAlaLeuSerGluAspLeuLeuSer 125
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
161 CTCACAATTCACAGCATCCAACGGATGCTTTATCAGAAGATCTGCTGAG 112
126 IleIleAlaAsnMetSerGlyCysLeuProTyTrpMetLeuProProLysCy 142
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
111 ATCATTGCAACT..... 100
142 sProAsnThrCysLeuAlaAsnLysTyTrpArgProIleThrGlyAlaCysA 159
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 .....GGCGAACAAATACAGCCCATCACAGGAGCTTGCA 66
159 snAsnArgAspHisProArgTrpGlyAlaSerAsnThrAlaIleAlaArg 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
65 ACAACAGAGACCCACCCAGATGGGCGCCTCCAACACAGCGCCTGGCACGA 16
176 TrpLeuProProVal 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
15 TGGCTCCCTCCAGTC 1
seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:us-08-840-551-6
seq_documentation_block:
; Sequence 6, Application US/08840551B
; Patent No. 6066449
; GENERAL INFORMATION:
; APPLICANT: Dittkoiff, Beth A., et al.
; TITLE OF INVENTION: METHOD OF DETECTING METASTATIC THYROID CANCER
; FILE REFERENCE: 0575/51662/jpw/jkm
; CURRENT APPLICATION NUMBER: US/08/840,551B
; CURRENT FILING DATE: 1997-04-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 169
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: OTHER NUCLEIC
US-08-840-551-6
alignment_scores:
  Quality: 259.00      Length: 56
  Ratio: 4.709
Percent Similarity: 98.214  Percent Identity: 98.214
alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-840-551-6 ..
Align seg 1/1 to: US-08-840-551-6 from: 1 to: 169
42 ValLeuGluGluSerLysArgLeuValAspThrAlaMetTyrrAlaThrMe 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GTCTTGGAGAAAGCAAGCGCCTGGTGGACCGCATGTACGCCAGCAT 50
58 tGlnArgAsnLeuLysArgGlyIleLeuSerGlyAlaGlnLeuLeuS 75
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 GCAGAGAAACCTCAAGAAAGAGGAATCCTTTCTCCAGCTCAGCTTCTGT 100
75 erPheSerLysLeuProGluProThrSerGlyValIleAlaArgAlaAla 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```





```
7831 ..... ||||| ||| |||||
392 AlaGlyAspGlyArgAlaSerGluValPro.....AATCCGACGGTACCCCTGCCGACCGAGTTCCTC 7863
7864 ACGGCAG.....CCGATCACCGGCTTCAACGAGAA 7895
402 .....SerLeuThrAlaLeuHisThrLeuTrpLeuArgGluHisA 415
7896 CTGTTGGGTGGCTGAGCATGCTCACCAGCTGTTCACTAAGGAGCACA 7945
415 snArgLeuAlaAlaLeuLysAlaLeuAsnAlaHisTrpSerAlaAsp 431
7946 ACGCCATCGCGCGATGCTCCAGCAGAAAGTACCCGACAAAGACGACCCAG 7995
432 AlaValTyrlngInGluAlaArgLysValValGlyAlaLeuHisGlnIleI 448
7996 TGGGTGTACGACCATGCGCGCTGCTCAACTCCGCGCTGATGGCCAAAGAT 8045
448 eThrLeuArgAspTyrIleProArgIleLeu..... 458
8046 CCACACCGTGAATGACCCCGCGCGGTATCCCAACCCGTCACCGAAC 8095
459 .....GlyProGlu... 461
8096 GCGCCATGATGCCAACTGGTGGGCGCTGCTGGGTCCGGTCCGGAGCGT 8145
462 ...AlaPheGlnGluTyrValGlyProTyrGluGlyTyrAspSerThrAl 477
8146 GACAAGTACCAAGGAGGCGCGCATGCTGCAGGAGGACCTGGCCAGCTC 8195
477 aAsnProThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyH 494
8196 CAACTCTTCCTCTCGCTCGCATTCCTGGCATCGACGCGCAGGCGCGCA 8245
494 isAlaThrIle...HisProLeuValArgArgLeuAspAlaSerPheGln 509
8246 GTTCGGCATCGACCATGCGCTGGCGCGCATGCTCGGCTCGAC... 8289
510 GluHisProAspLeuProGlyLeuTrpLeuHisGlnAlaPheSerPr 526
8290 ...AACCGCAACACTACGGCGT.....CC 8312
526 oTrpThrLeu.....LeuArgGlyGlyLeuAspProLeuI 539
8313 CTACACCTGACCGAGGAGTCTCGCGGTCTACCGCATGACCCGCTGA 8362
539 leArg.....GlyLeuLeuAlaArg 545
8363 TCGCGCAAGTGTGATGCTACGACATCGGCTCGAACAATCATCGCGCG 8412
546 ProAlaLysLeuGlnVal.....GlnAspGlnLeuMetas 557
8413 AGCGTCCGCTGCGAGAGACCGCGATGCGGACGCGGAGGAGCTGCTGC 8462
557 nGluGluLeuThrGluArgLeu.....PheValLeuSerAsnSerS 571
8463 GGACGAGAATCCCGAGCGCTGTGTACTCTCGGATCACCACCCCGG 8512
571 erThrLeu..... 573
8513 GCTCCTGACCTCAACACTACCGAACTTCTCGCGCAACCTGTCCATG 8562
574 .....AspLeuAlaSerIleAsnLeuGlnArgGlyAr 584
8563 CGCTGGTCGGCAACATGACCTCGGACCATCGAGTCTGTGTGACCG 8612
584 gasPheGlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeuP 601
8613 CGAGCGCGGGTGGCGCGCTACAAAGAGTTCGCGCGGAGATCGGCCTCA 8662
601 toArgLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSer 617
```

```
8663 ACCCGATCACCAAGTTGGAGACCTGACACCGACCGCCGACCTGGCC 8712
618 ValAlaAspLysIleLeu.....AspLeuTyrLysHisProAspAsnI 632
8713 AACCTCAAGCGCATCTACGCAACGACATCGAGAAG.....AT 8750
632 eAspValTrpLeuGlyLeuAlaGluAsnPhLeuPro 645
8751 TGACACCTGGTGGCATGCTGCGCGAGACCGTGGCTCG 8790
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-479-409-29
seq_documentation_block:
; Sequence 29, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; APPLICATION NUMBER: 08/911,853
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17612 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-479-409-29
alignment_scores:
Quality: 202.50 Length: 698
Ratio: 0.682 Gaps: 34
Percent Similarity: 42.550 Percent Identity: 22.350
alignment_block:
US-08-482-402a-3_COPY_1_848 x US-09-479-409-29 ..
Align seg 1/1 to: US-09-479-409-29 from: 1 to: 17612
58 MetGlnArgAsnLeuLysArgGlyIleLeuSerGlyAlaGlnLeuLe 74
7046 ATATGGCCCATGCCCCCTCCCGGGAGGGGGAGGGGGCGCGCAACTG 7095
74 userPheSerLysLeuProGlu...ProThrSerGlyValIleAla... 88
7096 CTTAATCTCCCGCTGCGCGGAAAGCGGCAAGCAACCCCATAGTACAA 7145
```

```

89 ..ArgAlaAlaGluIleMetGluThrSerIleGlnAlaMetIlysrGlys 104
||| |||||
7146 GAAGAAATCGGGAGATATCGCATGCTGTTGGTGCTACGTCGGCGGCT 7195
105 ValAsnLeuIlyThrGlnGlnSerGlnHisProThrAspAlaLeuSerG1 121
::: ::::: ||||| ::::: ||:::
7196 TGGTCAAGTTCGGACACCTGGCGCTGCTATGCGCGCTCATCAGCTCGCG 7245
121 uAspLeuLeuSerIleLeuAlaAsnMetSerGlyCysLeuProTyrMetL 138
: ||| ::: ::::: ::: |||
7246 C...TTGAGCGCGAGCTGCTGTTCAAGAACACCTGT .....TCGA 7283
138 euProProLysCysProAsnThrCysLeuAlaAsnLysTyrArgProIle 154
||||| ::::: ||||| ::::: |||||
7284 CGTCGACAACTGCGCGGGCGCAACCGCAGCATCACCCTGTGATGCCGCA 7333
155 ThrGlyAlaCysAsnAsnArgAspHisProArgTrpGlyAlaSerAsnTh 171
::: ||||| ::::: |||||
7334 GCC .....AGGTGGCGCTACCGAGGAC 7356
171 rAlaLeuAlaArgTrpLeuProProVal.TyrGluAspGlyPheSerGln 187
||| ||||| :::
7357 GCAC.....CCTGTAACAT..... 7370
188 ProArgGlyTyrAsnProGlyPheLeuTyrAsnGlyPheProLeuProPr 204
||||| ::::: ||||| ::::: |||||
7371 CCTCGC.....CAACCGGC.....CGAGGCTCGGTGTACCGCC 7405
204 oValArg.....Glu.ValThrArgHisValIleGlnVal 215
|:|||| ::: ||||| :::
7406 GCTTCGGCGCGCAAGCTCGACCCCGCGCTGACCCATGGCGAGACCGAGCC 7455
216 SerAsnGluValValThrAspAspArgTyrSerAspLeuLeuMetAl 232
7456 GACACCTGCTCAGTCCCAATCCGGGAGGTGAGTAACGTGCTGATGGC 7505
232 a.....T 233
↓
7506 CGGTGGCGAGTTCAAGCGCGCGCCAGCCTCAACTTCATCGCGCGCTCCT 7555
233 rpGlyGlnTyrIleAspHisasp...IleAlaPheThrProGlnSerThr 248
|| ||||| ::: |||||
7556 GGATCCAGTTTCATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7605
249 SerLysAlaAlaPheGlyGlySerAspCysGlnMetThrCysGluAs 265
:::
7606 GCCAAC..... 7611
265 nGlnAsnProCysPheProIleGlnLeuProGluGluAlaArgProAlaA 282
||||| ::::: |||||
7612 .....CGATCCAGGTGCGCTGCCGCTGCCGCGCGCGC 7645
282 laGlyThrAlaCysLeuProPheTyrArgSerSer..... 293
||||| ::: |||||
7646 TCGGCTCGCGCAGCTGTCGCTGCGCGCCAGCCAGCCGCGCGCGCT 7695
294 .....AlaAlaCysGlyThrGlyAspGlnGlyAlaLeuPheGlyAsnLe 308
||| :::::
7696 ACCCGCGCGCGCGCGC..... 7713
308 uSerThrAlaAsnProArgGlnGlnMetAsnGlyLeuThrSerPheLeuA 325
::: |||||
7714 .....AAGCGGGCCACTACCGCAACCAACACCCACTGCTGGTGG 7753
325 sPalaSerThrValTyrGlySerProAlaLeuGluArgGlnLeuArg 341
||||| ::::: |||||
7754 ATGGCTCGAGTTGTATGGCAGCAGCAGGACATCAACGACAAAGTGGCGC 7803
342 AsnTrpThrSerAlaGluGlyLeuLeuArgValHisGlyArgLeuArgAs 358
::: |||||
7804 .....GCCTTCGAGGGT.....GGCAAGCTGAAGAT 7829
358 pSerGlyArgAlaTyrLeuProPheValProArgAlaProAlaAlaC 375

```

```

7830 C..... 7830
375 ysAlaProGluProGlyAsnProGlyGluThrArgGlyProCysPheLeu 391
||||| |||
7831 .....ATCCGACAGGTACCTCGCGACCGAGTTCCTC 7863
392 AlaGlyAspGlyArgAlaSerGluValPro..... 401
::: |||
7864 AGCGGCAAG.....CCGATCACCGGCTTCAACGAGAA 7895
402 .....SerLeuThrAlaLeuHisThrLeuTrpLeuArgGluHisA 415
::: ||||| ::::: |||||
7896 CTGGTGGTGGCTGAGCATGTGCACCAGCTGTTCACTAAGGAGCACA 7945
415 snArgLeuAlaAlaAlaLeuLysAlaLeuAsnAlaHisTrpSerAlaAsp 431
|| ::::: |||||
7946 AGCCATCGCGCGATGCTCCACGAGAAGTACCAGGACGAGGACGAGCAG 7995
432 AlaValTyrGlnGluAlaArgLysValValGlyAlaLeuHisGlnIleI 448
::: ||||| ||| ::::: |||||
7996 TGGCTGTACGACCATCGCGCGCTGGTCAACTCCGCGCTGATGGCCAGAT 8045
448 eThrLeuArgAspTyrIleProArgIleLeu..... 458
| ::::: ||| :::::
8046 CCACACCGTGAATGACCCCGCGGTGATGCGCAACCCCGGTCAACGAA 8095
459 .....GlyProGlu... 461
8096 GCGCCATGATGCCAACTGGTGGGGCTGCTGGGTCCCGTCCGAGCGT 8145
462 ...AlaPheGlnTyrValGlyProTyrGluGlyTyrAspSerThrAl 477
::: ||||| :::
8146 GACAAGTACAGGAAGCGCGCATGCTGCAGGAGGACCTGGCCAGCTC 8195
477 asnProThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyH 494
||| ||| :::::
8196 CAACTCCTTCGCTCGCATCTCGGCATCGACGCGCAGCGCGCGCA 8245
494 isAlaThrIle...HisProLeuValArgArgLeuAspAlaSerPheGln 509
::: ||||| ||| :::::
8246 GTTCGGCCATCGACCATCGCTGGCGCGCATCGTCCGCTCGACC..... 8289
510 GluHisProAspLeuProGlyLeuTrpLeuHisGlnAlaPhePheSerPr 526
::: |||||
8290 ...AACCCGAACACTACGCGGTG.....CC 8312
526 otrThrLeu.....LeuArgGlyGlyLeuAspProLeuI 539
::: |||||
8313 CTACACCTGACCGAGGAGTTCGTCGCGGTCTACCGCATCGACCCGCTGA 8362
539 leArg.....GlyLeuLeuAlaArg 545
::: |||
8363 TCGCGCACAAGTTCGATGCTACGACATCGGCTCGAACATCATCGCGCGC 8412
546 ProAlaLysLeuGlnVal.....GlnAspGlnLeuMetAs 557
::: |||||
8413 AGCGTCCGCTGCAGGAGACCCCGCATGCGCGCGCGAGGAGCTGCTGGC 8462
557 nGluGluLeuThrGluArgLeu.....PheValLeuSerAsnSerS 571
::: |||||
8463 GGACGAGAATCCCGAGCGCTGTGGTACTCTTCGGCATCACCAACCCGG 8512
571 erThrLeu..... 573
::: |||
8513 GCTCGGTGACCTCAACAACATACCCGAATTCCTGCGCAACCTGTCCATG 8562
574 .....AspLeuAlaSerIleAsnLeuGlnArgGlyAr 584
||||| ::::: |||||
8563 CCGCTGGTCGGCAACATCGACCTGGGACCATCGAGTGTGTGTGACCG 8612
584 gAspHisGlyLeuProGlyTyrAsnGluTrpArgGluPheCysGlyLeuP 601
::: |||||

```



```

      ::::::::::|||
858 CTCGCGCTGATGCCAAGATCCACACCGTGAATGACCCCGCGGTGA 907
458 eu.....
908 TCGCAACCCGGTCACGACGCGCCATGATGCCAACTGGTGGGCGCTG 957
459 .....GlyProGlu.....AlaPheGlnTyrValGlyProTy 470
958 CTGGGTTCCGTCGGAGCGTGACAAGTACAGGAGGCGCGCATGCT 1007
470 rGluGlyTyrAspSerThrAlaAsnProThrValSerAsnValPheSer 487
1008 GCAGGAGGACTGCGCCAGCTCCAACTCTTCGTCCTCGCATTCGCGCA 1057
487 hrAlaAlaPheArgPheGlyHisAlaThrIle...HisProLeuValArg 502
1058 TCAGCGCAGCGCGGCGGATGTCGCGCATCGACATGCCCTGGCGCGC 1107
503 ArgLeuAspAlaSerPheGlnGluHisProAspLeuProGlyLeuTrpLe 519
1108 ATCGTCGGCTCGACC.....AACCCGAACAACATAGCGCGTG..... 1143
519 uHisGlnAlaPheSerProTrpThrLeu.....LeuArgG 532
1144 .....CCCTACACCTGACCGGAGGAGTTCGTCGCGG 1174
532 lyGlyGlyLeuAspProLeuIlearg..... 540
1175 TCTACCCGATGACCCCGCTGTCGCGCAGCAAGTGCATGTCTAGACATC 1224
541 .....GlyLeuLeuAlaArgProAlaLysLeuGlnVal..... 551
1225 GGCTCGACATCATCGCGCGCAGCGTCCGCTGCAGGAGACCCGCGATGC 1274
552 ....GlnAspGlnLeuMetAsnGluGluLeuThrGluArgLeu..... 564
1275 CGACGCGGAGGAGCTGTGGCGGACGAGAATCCCGAGCGCTGTGGTACT 1324
565 ..PheValLeuSerAsnSerSerThrLeu..... 573
1325 CCTTCGGCATCACCAACCCGGGCTCGTGTGACCCCTCAACAACATACCCGAAC 1374
574 .....AspLeuAlaLe 577
1375 TTCTGCGCAACCTGTCCATGCCGCTGTCGGCAACATCGACCTGGCGAC 1424
577 rIleAsnLeuGlnArgGlyArgAspHisGlyLeuProGlyTyrAsnGlu 594
1425 CATCGAGCTGTGTGACCGCGCGCGGCGCGGTGCCCGCTACAAACGAGT 1474
594 rPargGluPheCysGlyLeuProArgLeuGluThrProAlaAspLeuSer 610
1475 TCCGCGCGAGATCGGCTCAACCCCGATACCAAGTTGGAGGACCTGACC 1524
611 ThrAlaIleAlaSerArgSerValAlaAspLysIleLeu.....AspLe 625
1525 ACCGACCCGCGCCCTGCGCAACCTCAAGCGCATCTACGGCAACGACAT 1574
625 uTyrLysHisProAspAsnIleAspValTrpLeuGlyGlyLeuAlaGluA 642
1575 CGAGAAG.....ATTGACACCCCTGGTCGGCATGTGCGCCGAGA 1612
642 snPheLeuPro 645
1613 CCGTGGCTCGG 1623
```

seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:us-09-479-409-16

```

seq_documentation_block:
; Sequence 16, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
```

```

; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/479,409
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2742 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-479-409-16
```

```

alignment_scores:
  Quality: 195.00      Length: 587
  Ratio: 0.789        Gaps: 25
  Percent Similarity: 42.078  Percent Identity: 22.147
```

```

alignment_block:
US-08-482-402A-3_COPY_1_848 x US-09-479-409-16  ..
Align seg 1/1 to: US-09-479-409-16 from: 1 to: 2742
145 ThrCysLeuAlaAsnLysTyr.....ArgProIleThrGlyAlaCysAs 159
||||| |||:||||| ||| |||:|||||
151 ACCTGTGATGCCCCGACGACGAGGTGGCGGTACCGAGGACGCGACCTGTAA 200
||||| |||:||||| ||| |||:|||||
159 nAsnArgAspHisProArgTrpGlyAlaSerAsnThrAlaLeuAlaArg 176
| ||| |||:||||| ||| |||:|||||
201 CATCTCGCAACCCGCGCGAGGCTCGGTACCGCGCTTCGGGCGCA 250
||||| |||:||||| ||| |||:|||||
176 rPLeuProProValTyrGluAspGlyPheSerGlnProArgGlyTrpAsn 192
||| ||| |||:||||| ||| |||:|||||
251 AGCTGACACCCCGCGGTGACCCATGCGGAGACCGAGGCC..... 288
||| ||| |||:||||| ||| |||:|||||
193 ProGlyPheLeuTyrAsnGlyPheProLeuProValArgGluValTh 209
||| ||| |||:||||| ||| |||:|||||
289 .....GACACCTGCTCAGTCCCAATCCCGCGGAGGTGAG 323
||||| ||| |||:||||| ||| |||:|||||
209 rArgHisValIleGlnValSerAsnGluValValThrAspAspArg 226
||| ||| |||:||||| ||| |||:|||||
324 T...ACGTGCTGATGCGCGGTGGCGAG...TTCAAGCCGCGCCAGCC 367
||||| |||:||||| ||| |||:|||||
226 yrSerAspLeuLeuMetAlaTrpGlyGlnTyrIleAspHisAsp...Ile 241
||| ||| |||:||||| ||| |||:|||||
368 TCAACTTTCATCGCGCGCTCCTGGATCCAGTTCATGTCATGACTGGGTC 417
```



[illegible]

```

662 sAlaLeuArgAspGlyAspTrpPheTrpTrpGluAsnSerHisValPheT 679
    :::: :::: :::: :::: :::: :::: :::: :::: ::::
1712 TTCCTCCAGAG.....TACTGGAAGCGCAGCACATTTGGCG 1746
    :::: :::: :::: :::: :::: :::: :::: :::: ::::

679 hrAspAlaGlnArgArgGluLeuGluLysHisSerLeuArgValIle 695
    :::: :::: :::: :::: :::: :::: :::: :::: ::::
1747 GTGAGGTGGGCTTCAACCTTGTCAAGAGCGCCAGCTAAAGAAGCTGTT 1796
    :::: :::: :::: :::: :::: :::: :::: :::: ::::

696 CysAspAsnThr 699 .
    ||| |||||
1797 TGCCTCAACACC 1808

```

seq\_name: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-627-254C-26

```

seq_documentation_block:
; Sequence 26, Application US/08627254C
; Patent No. 5859229
;
; GENERAL INFORMATION:
;
; APPLICANT: Kniss, Douglas A.
;
; TITLE OF INVENTION: Eicosanoid Formation
;
; NUMBER OF SEQUENCES: 29
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Calfee, Halter & Griwold LLP
;
; STREET: 800 Superior Avenue
;
; CITY: Cleveland
;
; STATE: Ohio
;
; COUNTRY: USA
;
; ZIP: 44114
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/627,254C
;
; FILING DATE:
;
; CLASSIFICATION: 514
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Golrick, Mary E
;
; REGISTRATION NUMBER: 34,829
;
; REFERENCE/DOCKET NUMBER: 18525/00107
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (216) 622-8200
;
; TELEFAX: (216) 241-0816
;
; INFORMATION FOR SEQ ID NO: 26:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 2757 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: double
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA to mRNA
;
; HYPOTHETICAL: NO
;
; ANTI-SENSE: NO
;
; US-08-627-254C-26

```

```
alignment_scores:
    Quality: 178.50      Length: .   698
    Ratio: 0.553        Gaps:     42
    Percent Similarity: 46.275    Percent Identity: 21.633

alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-627-254C-26 ..

Align seg 1/1 to: US-08-627-254C-26 from: 1 to: 2757

137 MetLeuProPlyCysProAsnThrCysLeuAlaAsnLys.....Ty 151
:::|||||  |||:::  |||||:::
85 CTGCTGCCCG...ACACCCTGGTCTCTCCAGATCTCGGTGCC 131
:::|||||  |||:::  |||||:::
151 rArgPrfIleThrGlyAlaCys.....AsnAsnArgAspH 163
|||:::  ::|||
```

132 CTCACAGTCAATCCCTGTTGTTACTATCCGTCGCCAGAACACGAGGTGCT 181

163 isProAArgTPGlyAlaSerAsnThrAlaLeuAlaAArgTPLeuProPro 179

182 GTGTCGCTTTGGCTCGACAAC 204

180 ValTyrGlu.....AspGlyPheSerGlnProArg..... 189

205 ..TACCAGTGTGATTGTACTCGCAGCGGCTACTCAGGCCCACTGTAC 251

190 .....GlyTyr.....AsnProG 194

252 CATCCCTGAGATCGGACCTGGCTTGGAAATTCTCTGGCGGCCACGCCCT 301

194 lyPhe.....LeuTyrAsnGlyPheProLeu..... 202

302 CGTTACCCATTCTCTGTGACACATGATGCTCTGGGAATTTGTG 351

203 .....ProProValArgGluVal...ThrArgHisValIleGlnValSe 216

352 AATGCCACTTCATCCGAGAGAAGTACTATGCGCGCTGGTACTCACAGTGG 401

216 rAsnGluValValThrAspAspAspArgTyrSerAspLeu.....LeuM 231

402 GTCCCAACTTATCCCGACGCTCCGACCTACACACTCAGCGCATGACTACA 451

231 etAlaTrpGlyGlnTyr.....IleAspHisAspIleAlaPheThrPr 245

452 TCAGCTGGAGTCTCTCCAANTGTGAGCTACTATCTCGCATTCGTGCC 501

245 o.....GlnSerThrSerIysAlaAlaPheGly.....GlyGlySerA 258

502 TCTGTACCCAAAGACTGCCCCACACCCATGGGACCAAGGAAGAAACA 551

258 spCysGlnMetThrCysGluAsnGlnAsnProCys..... 269

552 GTTACCAGATTTACGCTTCTGGCCCAACAGCTGCTGTGAAAGGGAGT 601

270 ...PheProIleGlnLeuProGluAlaArgProAlaAlaGlyThrAl 285

602 TCATTC.....CTGCC.....CCAGGGCACCAACATC 630

285 aCysLeuProPheTyrArgSerSerAlaAlaCysGlyThrGlyAspGlnG 302

631 CTGTTTGCTTCTTTGGCAACACATTCACCC..... 661

302 lyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGlnGlnMet..A 318

662 .....ACCAGTTCTTCAAGACCTCTCGAAAGTGGGTC 694

318 snGlyLeuThrSerPheLeu.....AspAlaSerThrValTyr 330

695 CTGCTTTACCAAGCGCTTAGGCCACGGGTAGAGCTTGGCCACATTTAT 744

331 GlySerProAlaLeuGluArgGlnLeuArgAsnTPrThrSerAlaG 347

745 GGAGATAAT.....CTGGAACGACAGTATCACCTCGCGCTTCTCAAGA 788

347 uGlyLeuLeuArgValHisGlyArgLeuArgAspSerGlyArgAlaTyrL 364

789 TGGGAAACTTATAGGTAC.....CAGGTCTGGAC...GGAGAGGTGTACC 829

364 euProPheValProProArgAlaProAlaAlaCysAlaProGluProGly 380

830 CACCTTCGGT...GAACAGCGCGTCCGTGTGATGTCGCTACCCACGAGT 876

381 AsnProGlyGluThrArgGlyProCysPheLeuAlaGlyAspGlyArgAl 397

877 GTCCCGCTGAAGGCAG.....ATGCTGTGGGCCAGGAGGTGT 917

397 aSerGluValProSerLeuThrAlaLeuHisThrLeuTPrLeuArgGluH 414

918 TGGGTGCTTCCGGGGTGATGCTCTTCTCCACGATCTGGCTTCGTGAAC 967



```
414 isAsnArgLeuAlaAlaLeuLysAlaLeuAsnAlaHisTrpSerAla 430
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
968 ATAACCGGTGTGCGACCTGCTGAAGGAGGAGCATCCACGCTGGGATCAT 1017
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
431 AspAlaValTyrGlnGluAlaArgLysVal...ValGlyAlaLeuHisG1 446
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1018 GAGCAGCTCTCCAGACCATCTGCTCTATAGGAGAAACATCAA 1067
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
446 nIleIleThrLeuArgAspTyrIleProArgIleLeuGly..... 459
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1068 AATTGTC...ATTGAGGAGATGTGCGACACTTGAGTGGCTATTTCCTGC 1114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
460 .....ProGluAlaPheGlnGlnTyrValGlyProTyrGlu 471
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1115 AGCTCAAGTTTGACCGGAGCTGCTGTCGAGCGCCAGTCCCAATATCGA 1164
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
472 GlyTyrAspSerThrAlaAsnProThrValSerAsnValPheSerThrAl 488
:::|||||:|||||:|||||:|||||:|||||:|||||:
1165 .....AACCAGCAT 1172
|||||:|||||:|||||:|||||:|||||:|||||:
488 aAlaPheArgPheGlyHisAlaThrIleHisProLeuValArgLeuA 505
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1173 CGCATGGAATTTAACCATCTC..... 1194
|||||:|||||:|||||:|||||:|||||:|||||:
505 sAlaSerPheGlnGluHisProAspLeuProGlyLeu..... 517
|||||:|||||:|||||:|||||:|||||:|||||:
1195 .....TATCACTGCATCCACTCATGTCACCACTCTTCCCAAGTGGC 1236
|||||:|||||:|||||:|||||:|||||:|||||:
518 .....TrpLeuHisGlnAlaPhePheSerProTrpThrLeuLeuAr 531
:::|||||:|||||:|||||:|||||:|||||:|||||:
1237 TCACAAGAGTACAGCTACGAGCAGTGTATTTTAACTTCTATGCTGT 1286
|||||:|||||:|||||:|||||:|||||:|||||:
531 gGlyGlyGlyLeuAspProLeuIleArgGlyLeuLeuAlaArgProAlaL 548
|||||:|||||:|||||:|||||:|||||:|||||:
1287 GGACTATGGGTGTGAGCAGCTGGTG..... 1311
|||||:|||||:|||||:|||||:|||||:|||||:
548 ysLeuGlnValGlnAspGlnMetAsnGluLeuThrGluArgLeu 564
:::|||||:|||||:|||||:|||||:|||||:|||||:
1312 .....GATGCCCTCTCTGCCAGAGGCTGCCCGGAT 1344
|||||:|||||:|||||:|||||:|||||:|||||:
565 PheValLeuSerAsnSer.....ThrLeuAspLeuAlaSerIleAs 579
|||||:|||||:|||||:|||||:|||||:|||||:
1345 GGTGAGGTAGGAACCTTGACTATCATGCTCTGCTGCTGGCTGGATGT 1394
|||||:|||||:|||||:|||||:|||||:|||||:
579 nLeuGlnArgGlyArgAspHisGlyLeuProGlyTyrAsnGluTrpArg 596
|||||:|||||:|||||:|||||:|||||:|||||:
1395 CATCAAGGAGTCCCGAGAGATGCGCTTACAGCCCTTCAATGAATACCGAA 1444
|||||:|||||:|||||:|||||:|||||:|||||:
596 lUpheCysGlyLeuProArgLeuThrProAlaAspLeuSerThrAla 612
:::|||||:|||||:|||||:|||||:|||||:|||||:
1445 AGAGTTTGGCTTGAACCTTACACCTCTTCCAGGAGCTACACA..... 1488
|||||:|||||:|||||:|||||:|||||:|||||:
613 IleAlaSerArgSerValAlaAspLysIleLeuAspLeuTyrLysHisPr 629
|||||:|||||:|||||:|||||:|||||:|||||:
1489 ...GGAGAGAAGGAGATGGCTGCTGAGTTGGAGGAGCTGTACGCTGACAT 1535
|||||:|||||:|||||:|||||:|||||:|||||:
629 oAspAsnIleAspValTrpLeuGlyGlyLeuAlaGluAsnPheLeuProA 646
|||||:|||||:|||||:|||||:|||||:|||||:
1536 CGATGCTTAGAGTCTTACCCGGGGTGTCTGGAGAAGTGCACGCCA 1585
|||||:|||||:|||||:|||||:|||||:|||||:
646 rGla.....ArgThrGlyProLeuPheAlaCys 655
|||||:|||||:|||||:|||||:|||||:|||||:
1586 ACTCATCTTTGGAGAAGATGATAGATAGGAGGGGCTCCCTTTTCCCTC 1635
|||||:|||||:|||||:|||||:|||||:|||||:
656 .....LeuIleGlyLysGlnMetLysAlaLeuArgAspGlyAspTrpPh 670
|||||:|||||:|||||:|||||:|||||:|||||:
1636 AAGGGCTCTTAGGAATCCATCTGTTCCTCCAG..... 1671
|||||:|||||:|||||:|||||:|||||:|||||:
670 eTrpTrpGluAsnSerHisValPheThrAlaGlnArgArgLeuGlu 687
|||||:|||||:|||||:|||||:|||||:|||||:
1672 .TACTGGAACCCAGCAGCTGTGCGGTGTGAGTGGCTTCAACCTTGTC 1720
|||||:|||||:|||||:|||||:|||||:|||||:
687 687 luLysHisSerLeuSerArgValIleCysAspAsnThrGlyLeuThrArg 703
:::|||||:|||||:|||||:|||||:|||||:|||||:
1721 ACACAGCCTCACTGAAGAACTGGTCTGCCTCAACACC.....AAGACC 1764
|||||:|||||:|||||:|||||:|||||:|||||:
704 ValProMetAspAlaPheGlnValGlyLysPheProGluAspPheGluSe 720
|||||:|||||:|||||:|||||:|||||:|||||:
1765 TGCCCTATGTTCTTCGTGTGCCAGATTACCTGGAGATACCGGTC 1814
|||||:|||||:|||||:|||||:|||||:|||||:
720 rCysAspSerIleThrGlyMetAsnLeuGlu.....AlaTrp.... 732
|||||:|||||:|||||:|||||:|||||:|||||:
1815 TGTC.....TTAGTGAGAGCTCCACTGAGCTCTGAGGAGCTGGAAG 1858
|||||:|||||:|||||:|||||:|||||:|||||:
733 .....ArgGluThrPheProGlnAspAspLys 741
|||||:|||||:|||||:|||||:|||||:|||||:
1859 CAGCCTCTGGAGGAGGAGTGTTCCTCTGATGAGGACAAG 1899
|||||:|||||:|||||:|||||:|||||:|||||:
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-627-254C-28
seq_documentation_block:
; Sequence 28, Application US/08627254C
; Patent No. 5859229
; GENERAL INFORMATION:
; APPLICANT: Kniss, Douglas A.
; TITLE OF INVENTION: Eicosanoid Formation
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griwold LLP
; STREET: 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,254C
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Golrick, Mary E
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 18525/00107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8200
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2554 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-627-254C-28

alignment_scores:
Quality: 173.00 Length: 509
Ratio: 0.733 Gaps: 25
Percent Similarity: 46.365 Percent Identity: 21.415

alignment_block:
US-08-482-402A-3_COPY_1_848 x US-08-627-254C-28
Align seg 1/1 to: US-08-627-254C-28 from: 1 to: 2554
255 GlyGlySerAspCysGlnMetThrCysGluAsnGlnAsnProCysPhePr 271
|||||:|||||:|||||:|||||:|||||:
502 CGAAGAAGCAGTTGCCAGATG.....CC 524
```

```
271 oIleGlnLeuProGluAla.....Argp 280
| : : | | | : :
525 CAGCTCTGGCCCGCGCTTCTGCTCAGGAGAAAGTTTCATACCTGACCC 574
280 roAlaAlaGlyThrAlaCysLeuProPheTyArgSerSerAlaAlaCys 296
| | | | | | | | | | | | : : : : :
575 CCAAGGCACCACTCATGTTGCTTCTTTGGACACACACTTCACCCACC 624
297 GlyThrGlyAspGlnGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnPr 313
: : : : : : : : : : : : : : :
625 AGTTCT.....TCAAACTTCTGCACAGATGGGTCTCGCTTCACC 665
313 oArgGlnGlnMetAsnGlyLeuThrSer.....PheLeuAspAla..Ser 327
| | | | | | | | | | | : : : : :
666 AAGGCCTTGGGCCATGGGTAGACCTGGCCACACATTTATGGAGACATCT 715
328 ThrValTyGlySerSerProAlaLeu.....GluArgGlnLeu... 340
: : : : : : : : | | | | |
716 GGAGCGTCAGTATCACTCGCGCTCTTTAAGGATGGGAAATCAAGTACC 765
341 ...ArgAsnTrpThrSerAlaGluGlyLeuLeuArgValHisGlyArgL 356
| | | | | : : : : : : : :
766 AGGTGCTGGATGGAGAAATGTACCCGCCCTC..... 796
356 euArgAspSerGlyArg.....AlaTyLeuProPheValProProArg 370
| | | | | : : : : : : : :
797 .....GGTAGAAGAGCGCGCTGTGTGTGATGCACCTACCCCGGAGG 835
371 AlaProAlaAlaCysAlaProGluProGlyAsnProGlyGluThrArgG 387
| | | | | : : : : : : : :
836 CATCCC.....GCCACAGACAGATGCG..... 859
387 yProCysPheLeuAlaGlyAspGlyArgAla..SerGluValProSerLeu 403
: : : : | | | : : : : : : : :
860 .....TGTGGCCAGAGGTGTGTGGCTCTCTCTGGGCTC 896
404 ThrAlaLeuHisThrLeuTrpLeuArgGluHisAsnArgLeuAlaAl 420
| | | | | | | | | | | | | | |
897 ATGCTGTATGCCACGCTCTGGCTACGTGAGCACAACCGTGTGTGACCT 946
420 aLeuLyAlaLeuAsnAlaHisTrpSerAlaAspAlaValTyGlnGluA 437
| | | | | : : : : : : : : :
947 GCTGAAGGCTGAGCACCACCCACCTGGGCGATGAGCAGCTTTTCCAGAGA 996
437 laArgLysVal...ValGlyAlaLeuHisGlnIleIleThrLeuArgAsp 452
: : | : : : : : : : : : : :
997 CCCGCTCATCTCATAGGGAGACCATCAAGATTGTC...ATCGAGGAG 1043
453 TyrIleProArgIleLeuGly.....ProG 461
| | | : : : : : | | |
1044 TACGTGCAGCAGCTGAGTGGCTATTCTCTGCAGCTGAAATTTGACCCAGA 1093
461 uAlaPheGlnGlnTyValGlyProTyGluGlyTyArgSerThrAlaA 478
| : : : : : | | : :
1094 GCTGCTGTGCGGTCTCCAGTTCCCAATACCG..... 1124
478 snProThrValSerAsnValPheSerThrAlaAlaPheArgPheGlyHis 494
: : : : : : : : : : : :
1125 .....AACCGCATTCGATGGAGTTCAACCAT 1151
495 AlaThrIleHisProLeuValArgLeuAspAlaSerPheGlnGluH 511
: : : : : : : : : :
1152 CTC.....TACCCTGGCA 1165
511 sProAspLeuProGlyLeu.....TrpLeuHisG 521
| | | : : | | : :
1166 CCCCTCATGCTGACTCTCTCAAGTGGGCTCCAGGAGTACAGTACG 1215
521 lnAlaPhePheSerProTrpThrLeuLeuArgGlyGlyLeuAspPro 537
: : | | : : : : : : :
1216 AGCAGTTCTTGTTCACACCTCCATGTTGGTGACATATGGGGTTGAGGCC 1265
```

```
538 LeuIleArgGlyLeuLeuAlaArgProAlaLysLeuGlnValGlnAspG 554
| | : : :
1266 CTGGTG.....GA 1273
554 nLeuMetAsnGluLeuThrGluArgLeuPheValLeuSerAsnSerS 571
: : : : : : : : | | : :
1274 TGCCCTCTCTCCCGAGATTGCGCGGATCGGTGGGCGCAGGAACATGG 1323
571 ex.....ThrLeuAspLeuAlaSerIleAsnLeuGlnArgGlyArgAsp 585
: : | | : : : : : : : :
1324 ACCACCACATCTCGCATGTGGCTGTGATGTCATCAGGAGTCTCGGGAG 1373
586 HisGlyLeuProGlyTyTrpAsnGluTrpArgGluPheCysGlyLeuProAr 602
| | : : : : : : : : :
1374 ATCGGCTGACGCCCTTCAATGAGTACCGCAAGAGGTTTGGCATGAAACC 1423
602 gLeuGluThrProAlaAspLeuSerThrAlaIleAlaSerArgSerValA 619
: : : : : : : : : : :
1424 CTACACCTCTCTTCAGGAGCTC.....GTAGGAGAGAGGAGATGG 1464
619 laAspLysIleLeuAspLeuTyTrpLysHisProAspAsnIleAspValTrp 635
| : : : : : : : | | : :
1465 CAGCAGAGTTGGAGGAATGTATGGAGACATTGATCGGTGGAGTCTTAC 1514
636 LeuGlyGlyLeuAlaGluAsnPheLeuProArgAla..... 647
| | | | | : : : : :
1515 CCTGACTGCTTCTTGAAGTGCCTCAAACTCTATCTTTGGGGAGAG 1564
648 .....ArgThrGlyProLeuPheAlaCys.....LeuIleGlyLysG 660
| | | : : | | : : : :
1555 TATGATAGAGATTGGGCTCTCTTCTCAAGGCTCTCTTAGGGAATC 1614
660 InMetLysAlaLeuArgAspGlyAspTrpPheTrpTrpGluAsnSerHis 676
: : : : : : : : : :
1615 CCATCTGTCTCCGGAG.....TACTGGAGCGGACACACA 1649
677 ValPheThrAspAlaGlnArgArgGluLeuGluLysHisSerLeuSerAr 693
: : : : : : : : :
1650 TTTGGCGGGAGGTGGGCTTTAACAATTGTCAAGACGGCCACACTGAAGAA 1699
693 gValIleCysAspAsnThrGlyLeuThrArgValProMetAspAlaPheG 710
: : : : : | | | : :
1700 GCTGCTGCTGCTCAACAC.....AAGACCTGTCCTCTACGTTTCTCTCC 1743
710 InValGlyLysPheProGluAsp 717
: : | : : :
1744 GTGTCCCGGATCCAGTCAGGAT 1766

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-487-753-6

seq_documentation_block:
: Sequence 6, Application US/08487753
: Patent No. 5807733
: GENERAL INFORMATION:
: APPLICANT: Young, Donald A.
: APPLICANT: O'Banion, Michael K.
: APPLICANT: Winn, Virginia D.
: TITLE OF INVENTION: MAMMALIAN PROSTAGLANDIN H SYNTHASE-2
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
```





